

## **STIC Biotechnology Systems Branch**

### **RAW SEQUENCE LISTING** **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/552,909A  
Source: IFWP  
Date Processed by STIC: 11/7/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebs/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER:

10/552,909A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1        Wrapped Nucleics  
    Wrapped Aminos     The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
  
- 2        Invalid Line Length     The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
  
- 3        Misaligned Amino  
    J     Numbering     The numbering under each 5<sup>th</sup> amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
  
- 4        Non-ASCII     The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**
  
- 5        Variable Length     Sequence(s)        contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
  
- 6        PatentIn 2.0  
    "bug"     A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)       . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
  
- 7        Skipped Sequences  
    (OLD RULES)     Sequence(s)        missing. If intentional, please insert the following lines for **each** skipped sequence:  
                          (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                          (i)     SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                          (xi)  SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                          This sequence is intentionally skipped  
                          Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
  
- 8        Skipped Sequences  
    (NEW RULES)     Sequence(s)        missing. If **intentional**, please insert the following lines for **each** skipped sequence.  
                          <210> sequence id number  
                          <400> sequence id number  
                          000
  
- 9        Use of n's or Xaa's  
    (NEW RULES)     Use of n's and/or Xaa's have been detected in the Sequence Listing.  
                          Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.  
                          In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
  
- 10        Invalid <213>  
    Response     Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence. (see item 11 below)
  
- 11        Use of <220>     Sequence(s)        missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules
  
- 12        PatentIn 2.0  
    "bug"     Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
  
- 13        Misuse of n/Xaa     "n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid



IFWO

## RAW SEQUENCE LISTING

DATE: 11/07/2006

PATENT APPLICATION: US/10/552,909A

TIME: 11:51:44

Input Set : N:\RJAVED\10552909A.txt

Output Set: N:\CRF4\11072006\J552909A.raw

*see item 4 on Error  
summary sheet*

*supp 1, 3-4*

**Does Not Comply  
Corrected Diskette Needed**

*Since this is  
a patent  
document  
number,  
change  
to  
<3107>*

3 <110> APPLICANT: Xiao, Yingxao  
4 Feng, Xin-Hua  
6 <120> TITLE OF INVENTION: Gene expression suppression agents  
8 <130> FILE REFERENCE: 132848-01US  
10 <140> CURRENT APPLICATION NUMBER: US 10/552,909A  
11 <141> CURRENT FILING DATE: 2005-10-13  
13 <160> NUMBER OF SEQ ID NOS: 9  
15 <210> SEQ ID NO: 1  
16 <211> LENGTH: 27  
17 <212> TYPE: DNA  
18 <213> ORGANISM: Human  
20 <220> FEATURE:  
21 <221> NAME/KEY: primer\_bind  
22 <223> OTHER INFORMATION: Primer to amplify upstream promoter containing Box D in the  
23 Human 5S RNA gene  
W--> 25 <310> PATENT DOC NO: PCT/US2003/014631  
26 <311> PATENT FILING DATE: 2003-05-12  
W--> 27 <312> PUBLICATION DATE: PCT WO 2004/106488 A2  
29 <400> SEQUENCE: 1  
30 aacggatcca aaacgctgcc tccgcga 27  
32 <210> SEQ ID NO: 2  
33 <211> LENGTH: 25  
34 <212> TYPE: DNA  
35 <213> ORGANISM: Human  
37 <220> FEATURE:  
38 <221> NAME/KEY: primer\_bind  
39 <223> OTHER INFORMATION: Downstream reverse primer used to amplify the upstream  
40 promoter containing Box D in the Human 5S RNA gene. The  
41 sequence contains a PstI site at 7 bp upstream of the  
42 transcription site.  
44 <400> SEQUENCE: 2  
45 tagacgctgc aggaggcgcc tggct 25  
51 <210> SEQ ID NO: 3  
52 <211> LENGTH: 269  
53 <212> TYPE: DNA  
54 <213> ORGANISM: Human  
56 <220> FEATURE:  
57 <221> NAME/KEY: promoter  
58 <223> OTHER INFORMATION: Calculated BamHI-PstI fragment of the upstream promoter  
59 containing Box D in the Human 5S gene. Cloned into  
60 pBluescript-KS to give plasmid pPPVI.  
62 <400> SEQUENCE: 3  
63 ggatccaaaa cgctgcctcc gcgacagggc ggaggacgga gggcgtccca ggatcgtggg 60

*<300> insert this numeric identifier  
at the beginning of  
publication information.  
It never has a  
response.*

*this is  
for Publication Date  
use this format: yyyy-mm-dd*

## RAW SEQUENCE LISTING

DATE: 11/07/2006

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TIME: 11:51:44

Input Set : N:\RJAVED\10552909A.txt

Output Set: N:\CRF4\11072006\J552909A.raw

```

65 ccctgggcct gacgcctcgg agcactccct gctccgagcg ggcccgatgt ggtggaagct 120
67 cgggagcgcg ggagccgggg gaaggccgcg ggcagccgtc ggggggtcccc gatccgagcc 180
69 ccgcggcccc gggctggcgg tgctggctgc aatccggcgg gcacggccgg ccgggctggg 240
71 ctcttggggc agccaggcgc ctcttcag 269
73 <210> SEQ ID NO: 4
74 <211> LENGTH: 84
75 <212> TYPE: DNA
76 <213> ORGANISM: Human
78 <220> FEATURE:
79 <221> NAME/KEY: terminator
80 <223> OTHER INFORMATION: Comprises Box A, C and terminator of the human 5S RNA gene.
81     Serves as a top strand to anneal with SEQ ID NO: 5 to
82     create a double-stranded DNA molecule.
84 <400> SEQUENCE: 4
86 agaagacgaa gctaagcagg gtcgggcctg gttagtactt ggatgggaga ccgcctggga 60
88 ataccggtg ctgtaggctt ttg 84
91 <210> SEQ ID NO: 5
92 <211> LENGTH: 88
93 <212> TYPE: DNA
94 <213> ORGANISM: Human
96 <220> FEATURE:
97 <221> NAME/KEY: terminator
98 <223> OTHER INFORMATION: Comprises Box A, C and terminator of the human 5S RNA gene.
99     Serves as a top strand to anneal with SEQ ID NO: 4 to
100    create a double-stranded DNA molecule.
102 <400> SEQUENCE: 5
103 tcgacaaaaa gcctacagca cccggtattc ccaggcggtc tcccatccaa gtactaacca 60
105 ggcccgaccc tgcttagctt cgtcttct 88
108 <210> SEQ ID NO: 6
109 <211> LENGTH: 367
110 <212> TYPE: DNA
111 <213> ORGANISM: Human
113 <220> FEATURE:
114 <221> NAME/KEY: promoter
115 <223> OTHER INFORMATION: A BamHI-SalI fragment of plasmid pPPV2 containing the
116     upstream promoter containing Box D, A, C and the terminator
117     of the Human 5S gene.
119 <400> SEQUENCE: 6
120 ggatccaaaa cgctgcctcc gcgacagggc ggaggacgga gggcgtccca ggatcgtggg 60
122 ccctgggcct gacgcctcgg agcactccct gctccgagcg ggcccgatgt ggtggaagct 120
124 cgggagcgcg ggagccgggg gaaggccgcg ggcagccgtc ggggggtcccc gatccgagcc 180
126 ccgcggcccc gggctggcgg tgctggctgc aatccggcgg gcacggccgg ccgggctggg 240
128 ctcttggggc agccaggcgc ctcttcagg aattcgatag aagacgaagc taagcagggt 300
130 cgggcctggt tagtacttgg atgggagacc gcctgggaat accgggtgctg taggctttt 360
132 tgtcgac 367
134 <210> SEQ ID NO: 7
135 <211> LENGTH: 51
136 <212> TYPE: DNA
137 <213> ORGANISM: Human

```

## RAW SEQUENCE LISTING

DATE: 11/07/2006

PATENT APPLICATION: US/10/552,909A

TIME: 11:51:44

Input Set : N:\RJAVED\10552909A.txt

Output Set: N:\CRF4\11072006\J552909A.raw

139 <220> FEATURE:  
 140 <221> NAME/KEY: misc\_RNA  
 141 <223> OTHER INFORMATION: Contains designed siRNA sequence. Serves as a top strand  
 142 to anneal with SEQ ID NO: 8 to create a double-stranded DNA  
 143 molecule with PstI at the 5' end and BbsI at the 3' end.  
 145 <400> SEQUENCE: 7  
 W--> 146 gnnnnnnnnnn nnnnnnnnnn ntttcggnnn nnnnnnnnnn nnnnnntttt t 51  
 149 <210> SEQ ID NO: 8  
 150 <211> LENGTH: 59  
 151 <212> TYPE: DNA  
 152 <213> ORGANISM: Human  
 154 <220> FEATURE:  
 155 <221> NAME/KEY: misc\_RNA  
 156 <223> OTHER INFORMATION: Contains designed siRNA sequence. Serves as a top strand  
 157 to anneal with SEQ ID NO: 7 to create a double-stranded DNA  
 158 molecule with PstI at the 5' end and BbsI at the 3' end.  
 160 <400> SEQUENCE: 8  
 W--> 161 agctaaaaan nnnnnnnnnn nnnnnnnncc gaaannnnnnn nnnnnnnnnn nnnngctgca 59  
 163 <210> SEQ ID NO: 9  
 164 <211> LENGTH: 399  
 165 <212> TYPE: DNA  
 166 <213> ORGANISM: Human  
 168 <220> FEATURE:  
 169 <221> NAME/KEY: misc\_structure  
 170 <223> OTHER INFORMATION: A BamHI-SalI fragment of plasmid pPPV2 containing the siRNA  
 171 design. The second stretch of the 19 "n" bases are  
 172 complementary and reverse to the first stretch.  
 174 <400> SEQUENCE: 9  
 175 ggatccaaaa cgctgcctcc ggcacagggc ggaggacgga gggcgctcca ggatcgtggg 60  
 177 ccctgggcct gacgcctcgg agcactccct gctccgagcg ggcccgatgt ggtggaagct 120  
 179 cgggagcgcg ggagccgggg gaaggccgcg ggcagccgctc gggggctccc gatccgagcc 180  
 181 ccgcggcccc gggtcgccgg tctcggtctc aatccggcgg gcacggccgg ccgggctggg 240  
 W--> 183 ctcttggggc agccagggcg ctccttcagc nnnnnnnnnn nnnnnnnnt ttcggnnnnn 300  
 185 nnnnnnnnnn nnnnttttta gctaagcagg gtcgggcctg gttagtactt ggatgggaga 360  
 187 ccgcctggga ataccgggtg ctgtaggctt tttgtcgac 399

n's need  
 explanation. see  
 p. 4 for  
 even  
 explanation

see p. 4

OK, but all the n's  
 need

explanation,  
 further,

which  
 bases do  
 these n's  
 represent?

FYI: all nucleotides  
 MUST be in  
 lower-case  
 letters

(see 1.823 of  
 Sequence Rules)  
 and p. 4

## VARIABLE LOCATION SUMMARY

DATE: 11/07/2006

PATENT APPLICATION: US/10/552,909A

TIME: 11:51:45

Input Set : N:\RJAVED\10552909A.txt

Output Set: N:\CRF4\11072006\J552909A.raw

Use of n's or Xaa's (NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.

Use of &lt;220&gt; to &lt;223&gt; is MANDATORY if n's or Xaa's are present.

in <220> to <223> section, please explain location of n or Xaa, and which  
residue n or Xaa represents.

Seq#:7; N Pos. 3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,28,29,30  
Seq#:7; N Pos. 31,32,33,34,35,36,37,38,39,40,41,42,43,44,45,46  
Seq#:8; N Pos. 10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,35  
Seq#:8; N Pos. 36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53  
Seq#:9; N Pos. 271,272,273,274,275,276,277,278,279,280,281,282,283,284,285  
Seq#:9; N Pos. 286,287,288,289,296,297,298,299,300,301,302,303,304,305,306  
Seq#:9; N Pos. 307,308,309,310,311,312,313,314

## VERIFICATION SUMMARY

DATE: 11/07/2006

PATENT APPLICATION: US/10/552,909A

TIME: 11:51:45

Input Set : N:\RJAVED\10552909A.txt

Output Set: N:\CRF4\11072006\J552909A.raw

L:25 M:284 W: Blank Line not Allowed, <310> field identifier  
L:27 M:256 W: Invalid Numeric Header Field, Wrong PUBLICATION DATE:YYYY-MM-DD  
L:146 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:7  
L:146 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0  
L:161 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:8  
L:161 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0  
L:183 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:9  
L:183 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:240  
L:183 M:112 C: (48) String data converted to lower case,  
M:341 Repeated in SeqNo=9